

Run on:	July 26, 2005, 10:42:32 ;	Search time 164 Seconds (without alignments)
Title:	US-09-147-490-1	
Perfect score:	58	
Sequence:	1 LVVRYWTQRF 10	
Scoring table:	BLOSUM62	
	Gapext 10.0 , Gapext 0.5	
Searched:	2105692 seqs , 388760381 residues	
Copyright (c) 1993 - 2005 Compugen Ltd.	Gendcore version 5.1.6	
DM protein - protein search, using SW model		
Run on:	23.583 Million cell updates/sec	

ALIGNMENTS

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneset_1.6Dec04:
 1: geneset_1980s: *
 2: geneset_1990s: *
 3: geneset_2000s: *
 4: geneset_2001s: *
 5: geneset_2002s: *
 6: geneset_2003s: *
 7: geneset_2003s: *
 8: geneset_2004s: *

RESULT 1
 AAR97348
 ID AAR97348 standard; protein; 10 AA;
 XX
 AC AAR97348;
 XX
 DT 17-OCT-1996 (first entry)
 XX
 DB Peptide fragment of haemoglobin B (Haemorphin 10).

KW haemoglobin; INPROL; stem cell proliferation; B lymphocytes; B cells;
 chemotherapy; Cancer; haematopoietic cells; marrow; blood;
 KW myeloproliferative disease; autoimmune disease; adjuvant; vaccination;
 KW immunodepression; gene therapy.

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	58	100.0	10	2	AAR97348	Peptide f
2	58	100.0	10	2	AAW30318	Peptide h
3	58	100.0	10	2	AAW37247	Angiotensin
4	58	100.0	10	4	AAU71993	Anti-atre
5	58	100.0	10	5	ABG31639	Hemorphin
6	58	100.0	10	6	ABP72839	Angiotensins
7	58	100.0	12	6	AAO30111	Human bet
8	58	100.0	74	1	AAP50291	Sequence
9	58	100.0	74	2	AAR6562	Human bet
10	58	100.0	86	4	AAO07245	Human pol
11	58	100.0	104	4	AAU30074	Novel hum
12	58	100.0	110	4	Aao0538	Human pol
13	58	100.0	112	2	Aar82261	Human bet
14	58	100.0	112	2	Aar89262	Human bet
15	58	100.0	121	3	AAG01752	Human sec
16	58	100.0	124	4	AAU29698	Novel hum
17	58	100.0	127	4	Aao13066	Human pol
18	58	100.0	128	4	Aao09585	Human pol
19	58	100.0	130	6	ABR82319	Ruman met
20	58	100.0	137	4	AAU30769	Novel hum
21	58	100.0	140	4	AAM79250	Human pro
22	58	100.0	140	5	ABP63040	Human pol
23	58	100.0	141	2	AAW30718	Haemoglobin
24	58	100.0	142	4	AAU29784	Novel hum
25	58	100.0	143	4	AAU30030	Novel hum

XX Homo sapiens.
 XX OS
 XX WO9610634-A1.
 XX PN
 XX PD 11-APR-1996.
 XX PF 95WO-US012268.
 XX PF 29-SEP-1995;
 XX PR 94US-00316424.
 XX PR 28-SEP-1995;
 XX PA (PRON-) PRO-NEURON INC.
 XX PI Kozlov V, Tsvylova I, Wolpe SD;
 XX DR 1996-209356/21.
 XX PT Inhibitors of stem cell proliferation comprising haemoglobin chains -
 PT useful in mammals, e.g. for protecting stem cells from anti-viral agents,
 PT treating cancer, and maintaining mammalian haematopoietic stem cells ex
 vivo.
 XX
 PS Claim 17, Page 65, 101pp; English.
 XX Compositions (INPROL) comprising a polypeptide selected from the
 CC haemoglobin alpha, beta, gamma, delta, epsilon or zeta chains and a
 CC carrier may be used to inhibit stem cell proliferation. INPROL can also
 CC be used for stimulating the growth of B cells and can be used with ratio-
 CC or chemotherapy to treat cancer in mammals by differentially protecting
 CC normal stem cells and not cancer cells from such therapy. INPROL is also
 CC useful for maintaining mammalian haematopoietic stem cells *ex vivo*
 CC (particularly bone marrow, peripheral blood or cord blood cells); for the
 CC *ex vivo* expansion of haematopoietic cells when used in combination with a

CC stimulatory cytokine. INPROL can also be used to treat myeloproliferative
 CC or autoimmune disease. INPROL is also useful as an adjuvant in the
 CC vaccination of mammals and can be used to treat a mammal with
 CC immunodepression caused by stem cell proliferation. INPROL can also be
 CC used in gene therapy. This peptide fragment of human haemoglobin B
 CC corresponds to amino acids 32-41 of the mature protein given in AAR97358
 XX

SQ Sequence 10 AA;

	Query Match	Score	DB	Length	0;
Best Local Similarity	100.0%	2;			
Matches 10;	Conservative	Pred. No.	0.0015;		
Mismatches 0;		Nimatches	0;	Indels	0;
Gaps 0;					

Qy 1 LVVYFWTQRF 10
 Db 1 LVVYFWTQRF 10

RESULT 2

ID	AAW30318 standard; peptide; 10 AA.
XX	
AC	AAW30318;
XX	
DT	20-APR-1998 (first entry)
XX	
DE	Peptide haemorphin 10 with opiate activity.
XX	
KW	INPROL; stem cell; inhibition; stimulation; proliferation; myoglobin;
KW	alpha chain; haemoglobin; radiotherapy; chemotherapy; cancer;
KW	differential protection; stem cell hypoproliferation; aplastic anaemia;
KW	stem cell exhaustion; haemorphin; opiate activity.
XX	
OS	Synthetic.
OS	Home sapiens.
XX	
PN	WO9736922-A1.
XX	
PD	09-OCT-1997.
XX	
PF	03-APR-1997; 97WO-US005601.
XX	
PR	03-APR-1996; 96US-00627173.
XX	
PA	(PRON-) PRO-NEURON INC.
XX	
PI	Wolpe SD, Tsvirova I;
XX	
DR	WPI 1997-50344/46.
XX	
PT	Haemoglobin alpha chain derivatives - used to inhibit or stimulate stem
PT	cell proliferation, for treatment of cancer, immune depression etc.
XX	
PS	Claim 49: Page 117: 162PP; English.
XX	
CC	The present peptide is derived from amino acids 32-41 of the beta chain
CC	of adult human haemoglobin. The peptide has sequence similarity and
CC	biological activity similar to other atypical opiate peptides. The
CC	peptide can stimulate or inhibit stem cell proliferation, similar to
CC	INPROL compounds. The peptide is used to inhibit stem cell proliferation,
CC	particularly during radiotherapy or chemotherapy of cancer, but more
CC	generally wherever a mammal is exposed to an agent, e.g. an antiviral,
CC	which damages or destroys stem cells. It can also be used for differential
CC	protection of normal stem cells, but not cancer cells, from chemotherapy
CC	or radiation, particularly after normal stem cells have been induced to
CC	proliferate by therapeutic treatment. The peptide can also be used for
CC	control of stem cell hypoproliferation (e.g. aplastic anaemia), for
CC	treatment or preventing stem cell exhaustion (e.g. where caused by
CC	acquired immune deficiency syndrome), and to treat or prevent
CC	immunodeficiency. INPROL can also be used for treating pain in a mammal.
CC	INPROL and related compounds reversibly inhibit or stimulate stem cells
CC	depending on the dose, so allow precise control over cycling of these
CC	cells

RESULT 4

AAU79893 standard; peptide; 10 AA.

ID AAU79893;

AC AAU79893;

XX DT 15-JUL-2002 (first entry)

XX DE Anti-stress agent and anti-stress food associated peptide #5.

XX KW Anti-stress agent; anti-stress food; anxiolytic; tranquiliser; stress.

OS Synthetic.

XX PN JP2001226281-A.

XX PD 21-AUG-2001.

XX PP 10-FEB-2000; 20000JP-00033569.

XX PR 10-FEB-2000; 20000JP-00033569.

XX PA (ITOH-) ITO HAM KK.

XX DR WPI; 2001-609888/70.

XX PT An anti-stress agent and an anti-stress food.

XX Disclosure; Page 2; 7pp; Japanese.

PS The invention describes an anti-stress agent containing a peptide and/or its pharmacologically allowable salt as the active component. The anti-stress agent and the anti-stress food function as anxiolytics and tranquillisers and can be used for decreasing and preventing mental and physical symptoms caused by various stresses. This sequence represents a peptide included in the anti-stress agent and the anti-stress food of the invention.

XX SQ Sequence 10 AA;

Query Match	100.0%	Score 58;	DB 4;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.0015;		
Matches	10;	Conservative	0;	Mismatches 0;
			Indels 0;	Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10

RESULT 5

ABG31639 standard; peptide; 10 AA.

ID ABG31639;

AC ABG31639;

XX DT 29-NOV-2002 (first entry)

DB Hemorphin ligand LVV-H-7 peptide.

XX KW Human; bombesin receptor subtype 3; BRS-3; receptor; hemorphin ligand; Vv-H-7; LVV-H-7; cell growth; cell proliferation; tumour development; cancer; small cell lung carcinoma; SCLC; neoplasm; immunology; inflammation; genitourinary system; cytotoxic; antiinflammatory; immunomodulator; bombesin antagonist; bombesin agonist; vaccine; gene therapy.

OS Synthetic.

XX PN WO200263305-A2.

XX PD 15-AUG-2002.

XX 31-JAN-2002; 2002WO-EP000978.

XX PR 02-FEB-2001; 2001EP-0010383.

XX PR 08-FEB-2001; 2001US-0267186P.

XX PA (SOLVAY PHARM GMBH).

XX PI Lammerich H, Busmann P, Kutzleb C, Wendland M, Seiller P;

XX PI Berger C, Eickelmann P, Meyer M, Forssmann W, Maronde E;

XX DR WPI; 2002-627570/6.

XX PT Determining if a substance is a potential ligand of a bombesin receptor subtype 3 (BRS-3), useful for preparing a composition for treating e.g. cancer, comprises contacting cell expressing the BRS-3 polypeptide with hemorphin ligands.

XX PS Example 2; Page 12; 64pp English.

XX CC The present invention relates to a new method of determining if a substance is a potential ligand of a bombesin receptor subtype 3 (BRS-3) polypeptide receptor. The method of the invention involves contacting cells expressing the BRS-3 polypeptide receptor, or a receptor membrane preparation comprising the BRS-3 polypeptide receptor, with labelled hemorphin ligands Vv-H-7 or Lvv-H-7 in the presence and in the absence of the substance, and measuring the binding of the ligand to the receptor.

CC The compound or the antagonist is useful for preparing a pharmaceutical composition for the treatment and/or prophylaxis of BRS-3/hemorphin ligand based dysfunctions, disorders or diseases that are related to cell growth, cell proliferation, tumour development and cancer, preferably or to genitourinary system, or to any other dysfunction, disorder or disease related to the activities of BRS-3, in particular of BRS-3, in connection with its interrelation with Vv-H-7 and/or Lvv-H-7. The protein-ligand complex is useful for the design and modulation or optimisation of lead structures with BRS-3 polypeptide-binding activity. The validated animal models are useful for evaluating identified agonists or antagonists at BRS-3 polypeptide receptor in dysfunctions, disorders or diseases. The BRS-3 polypeptide is useful in diagnosing the diseases mentioned, or a subject's susceptibility to it, and in screening methods for identifying the compound, antagonist or agonist. The present amino acid sequence represents the hemorphin ligand Lvv-H-7 Peptide that was used in the methods of the invention.

XX SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

0;

Mismatches 0;

Indels 0;

Gaps 0;

SQ Sequence 10 AA;

Query Match

100.0%; Score 58;

DB 5;

Length 10;

Best Local Similarity

100.0%;

Pred. No. 0.0015;

Matches

10;

Conservative

XX	13-FEB-2003 .	OS	Homo sapiens.
PD		XX	
XX	02-AUG-2002; 2002WO-AU001034 .	PN	WO2003046556-A2.
PP		XX	
XX	02-AUG-2001; 2001AU-00006772 .	PD	05-JUN-2003 .
PR		XX	
XX	17-OCT-2001; 2001US-03130170P .	PF	31-OCT-2002; 2002WO-CA001657 .
PR		XX	
(FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY .		PR	23-NOV-2001; 2001US-00993343 .
PA		XX	
XX		PA	(SYN-X) SYN-X PHARMA INC.
PI	Albiston AL, McDowall SG, Mendelsohn FAO, Chai SY;	XX	
XX		XX	
DR	WPI; 2003-278368/27 .	PI	Jackowski G, Marshall J;
XX		XX	
PT	Modulating the expression, production or activity of AT4 receptor/insulin	DR	2003-523251/49 .
PT	-regulated aminopeptidase (IRAP) for preventing or treating e.g.,	PT	
PT	Parkinson's disease, comprises administering a modulator of AT4	PT	
PT	receptor/IRAP .	XX	
XX		PT	Novel biopolymer marker or its analyte, useful for evidencing and
		PT	categorizing at least one disease state in a patient .
		XX	
PS	Claim 26; Page 102; 146pp; English .	PS	Claim 1; Page 43; 43pp; English .
XX		PS	
CC	The present sequence is that of a peptide isolated from the sheep	CC	The invention relates to a biopolymer marker or its analyte, useful for
CC	cerebral cortex. This decapeptide binds with nanomolar affinity to the	CC	evidencing and categorising at least one disease state in a patient. The
CC	angiotensin IV (AT4) receptor and which mimics the actions of human AT4.	CC	invention particularly relates to Globin biopolymer markers indicative of
CC	The AT4 receptor has been identified insulin-regulated aminopeptidase	CC	insulin resistance. Biopolymer marker is useful for evidencing and
CC	(IRAP). The invention provides a method of screening for compounds which	CC	categorising at least one disease state e.g., for predicting insulin
CC	can modulate the activity of the AT4 receptor/IRAP. The compound is: a	CC	resistance. A diagnostic assay kit is useful for identifying therapeutic
CC	ligand of AT4 receptor/IRAP, such as the present decapeptide; an	CC	avenues related to a disease state. Biopolymer markers are useful as
CC	oligonucleotide that is antisense to a nucleic acid encoding AT4	CC	tools for rapidly and accurately diagnosing acute Syndrome X events such
CC	receptor/IRAP; or a compound that is able to modulate the cellular	CC	as heart attack and stroke, and facilitate treatment. The present
CC	localisation of AT4 receptor/IRAP. The compound can be used to: treat or	CC	sequence is human beta globin biopolymer marker peptide indicative of
CC	prevent a disorder of the central nervous system associated with dementia	CC	insulin resistance
CC	and/or memory loss, motor and sensory systems, trauma or stroke, or	XX	
CC	disorder of the cardiovascular system, development and/or growth, glucose	SQ	Sequence 12 AA;
CC	and fat metabolism, reproductive tract, cancer or a disorder associated	Query Match	100.0%; Score 58; DB 6; Length 12;
CC	with degenerative condition selected from motor neuron	Best Local Similarity	100.0%; Pred. No. 0.0018;
CC	disease (amyotrophic lateral sclerosis), progressive spinal muscular	Matches	0; Mismatches 0; Indels 0; Gaps 0;
CC	atrophy, infantile muscular atrophy, Charcot-Marie-Tooth disease,	Qy	1 LVVYPWTQRF 10
CC	Parkinson's disease, Parkinson-Plus syndrome, Guamanian Parkinsonian	Db	3 LVVYPWTQRF 12
CC	dementia complex, progressive bulbar atrophy and Alzheimer's disease, a		
CC	neurodegenerative condition arising from ischaemia, hypoxia, neural		
CC	injury, surgery or exposure to neurotoxins, a peripheral sensory	RESULT 8	
CC	neuropathy resulting from exposure to drugs, toxins or to diabetes, a	ID	AAP50291
CC	condition characterised by neuronal deficit or neuronal death and also	ID	AAP50291 standard; protein; 74 AA.
CC	memory disorders and memory loss; enhance memory and/or learning; to	AC	AAP50291;
CC	modulate in vivo uptake of glucose into cells or tissues; and to	XX	XX
CC	stimulate growth in an animal, especially a farm animal (all claimed).	XX	XX
CC	Note: The present sequence is identified as SEQ ID 2 in Claim 26, but is	XX	XX
CC	SEQ ID 3 in the sequence listing	XX	XX
XX	Sequence 10 AA;	XX	XX
XX		XX	XX
Query Match	100.0%; Score 58; DB 6; Length 10;	XX	XX
Best Local Similarity	100.0%; Pred. No. 0.0015;	XX	XX
Matches	0; Mismatches 0; Indels 0; Gaps 0;	DE	Sequence encoded by second exon of rabies glycoprotein gene.
Qy	1 LVVYPWTQRF 10	KW	Rabies vaccine; therapy; glycoprotein; antigen; diagnosis.
Db	1 LVVYPWTQRF 10	XX	XX
		OS	Rabies virus.
		XX	XX
		PN	WO8501516-A.
RESULT 7		XX	
AAO30111		XX	
ID	AAO30111 standard; peptide; 12 AA.	PD	11-APR-1985 .
XX		XX	PR 03-OCT-1983;
XX		XX	PR 27-MAR-1984;
DT	03-SEP-2003 (first entry)	PR 03-OCT-1984;	
XX		XX	PR 84FR-00004754 .
XX		XX	84FR-00015716 .
DE	Human beta globin biopolymer marker peptide.	PP	03-OCT-1983;
XX		XX	(TRGF-) TRANSGENE SA.
XX		PA	(LATH-) LATHE R.
XX		PA	Human; biopolymer marker; disease categorization; insulin resistance;
XX		PA	acute syndrome X; heart attack stroke; therapy; beta globin.

PI Lathe R, Kienny MP, Lemoine Y, Loison G, Aigle M;
 XX WPI: 1985-098845/16.
 DR N-PSDB; AAN50333.
 XX Vector for expressing rabies antigen - in eucaryotic cells, useful for
 PT making vaccines and curative agents.
 PT
 XX Example: Fig 10; 62pp; French.

XX inventors claim a vector for expressing a rabies antigen protein in
 CC eucaryotic cells. After glycosylation with a yeast (specifically at ASP
 CC residues 204 and 319), the recombinant antigen protein is useful as a
 CC vaccine or curative agent. The coding sequence in the vector can be
 CC followed by an intron (see AAN50333, N50334) or sites of Polyadenylation.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 74 AA;

```
Query Match 100.0%; Score 58; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LVVYPPTQRF 10
    ||||| | |
  2 LVVYPPTQRF 11
```

RESULT 10
 AAO07245

ID AAO07245 standard; protein; 86 AA.

AC AAO07245;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 21137.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

DE Homo sapiens.

XX OS WO200164835-A2.

XX PN

XX PD 07-SEP-2001.

XX PP 26-FEB-2001; 2001WO-US004927.

XX PR 28-FEB-2000; 2000US-00515126.

XX PR 18-MAY-2000; 2000US-00577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI: 2001-514838/56.

XX DR N-PSDB; AA187176.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX Claim 20; SEQ ID NO 21137; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI193841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 86 AA;

CC respectively. These pairs of sequences may be compared for differences.
 CC Optimised human beta-globin coding sequences for exons 1, 2 and 3 are
 CC depicted in AAO83722, AAO83723 and AAO83724, respectively. These
 CC sequences may be compared with AAQ83716, AAQ83717 and AAQ83718
 CC respectively. The AA sequences encoded by the optimised human beta-globin
 CC coding sequences are given in AAR65601, AAR65602, AAR65603. (Updated on
 CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 74 AA;

```
Query Match 100.0%; Score 58; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.012; Indels 0; Mismatches 0; Gaps 0;
```

Qy 1 LVVYPPTQRF 10
 ||||| | |
 2 LVVYPPTQRF 11

RESULT 9
 AAR69602

ID AAR69602 standard; protein; 74 AA.

AC AAR69602;

XX DT 25-MAR-2003 (revised)

XX DT 25-SEP-1995 (first entry)

XX DB Human beta-globin encoded by optimised exon 2.

XX Beta-globin; optimised codons; exon 2.

XX Synthetic.

XX OS WO9504744-A1.

XX PN

XX PD 16-FEB-1995.

XX PP 29-JUL-1994; 94WO-US008630.

XX PR 11-AUG-1993; 93US-00105939.

XX PA (DNXD-) DNX CORP.

XX PI Kumar R, Sharma A, Paulhac C, Khoury-Christiansen AM, Midha S;

XX DR WPI: 1995-090838/12.

XX N-PSDB; AA083723.

XX Production of human haemoglobin in transgenic pigs - by introducing gene

PT constructs comprising human alpha and beta globin genes into pig ova, for

PT an efficient source of haemoglobin for use in e.g. transusions.

XX Example: Fig 39; 155pp; English.

XX Human alpha-globin is expressed in transgenic pigs at higher levels than

CC human beta-globin. One approach to increasing the level of expressed beta

CC -globin is to engineer the human beta-globin gene from the promoter

CC region through the coding sequence and into the polyA site and 3' UTR to

CC be similar to pig beta-globin gene, but without altering the AA sequence

CC from that of authentic wt human beta-globin. PCR was used to optimise

CC human beta-globin gene for porcine expression. Equivalent fragments of

CC the human and pig beta-globin coding sequences in exons 1, 2 are 3 are

CC depicted in AAQ83716/Q83719, AAQ83717/Q83720 and AAQ83718/Q83721,

Qy	1 LVVYPNTQRF 10 39 LVVYPNTQRF 48	Query Match Score 58; DB 4; Length 86; Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;	RESULT 11 AAU30074 ID AAU30074 standard; protein; 104 AA. XX AC AAU30074; XX DT 18-DEC-2001 (first entry) XX DE Novel human secreted protein #565. XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia. XX OS Homo sapiens. XX PN WO200179449-A2. XX PD 25-OCT-2001. XX PF 16-APR-2001; 2001WO-US008656. XX PR 18-APR-2000; 2000US-00558929. XX PR 26-JAN-2001; 2001US-00770160. XX PA (HYSEQ -) HYSEQ INC. XX PI Tang YT, Liu C, Drmanac RT; XX DR WPI; 2001-514838/56. N-PSDB; AAI82469. XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders. XX PS Claim 20; SEQ ID NO 16430; 1399pp + Sequence Listing; English. XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to cytotoxic, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, immunomodulatory activity and immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences	RESULT 12 AAU02538 ID AAU02538 standard; protein; 110 AA. XX AC AAU02538; XX DT 06-NOV-2001 (first entry) XX DE Human polypeptide SEQ ID NO 16430. XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. XX OS Homo sapiens. XX PN WO200164835-A2. XX PD 07-SEP-2001. XX PR 26-FEB-2001; 2001WO-US004927. XX PR 28-FEB-2000; 2000US-00515126. PR 18-MAY-2000; 2000US-00577409. XX PA (HYSEQ -) HYSEQ INC. XX PI Tang YT, Liu C, Drmanac RT; XX DR WPI; 2001-514838/56. N-PSDB; AAI82469. XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders. XX PS Claim 20; SEQ ID NO 16430; 1399pp + Sequence Listing; English. XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to cytotoxic, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences	RESULT 13 AAR9261 ID AAR9261 standard; peptide; 112 AA. XX AC AAR9261; XX DT 25-MAR-2003 (revised) DT 04-MAR-1996 (first entry)
Db	Sequence 104 AA;	Query Match Score 58; DB 4; Length 110; Best Local Similarity 100.0%; Pred. No. 0.019; Mismatches 0; Indels 0; Gaps 0;	Qy 1 LVVYPNTQRF 10 33 LVVYPNTQRF 42		
Db	Sequence 104 AA;	Query Match Score 58; DB 4; Length 104; Best Local Similarity 100.0%; Pred. No. 0.019; Mismatches 0; Indels 0; Gaps 0;	Qy 1 LVVYPNTQRF 10 33 LVVYPNTQRF 42		

DE Human beta-globin mutant Gln/Lys90 and Asp108.
 XX Human beta-globin; mutant Gln/Lys90 and Asp108; hypoxic cells;
 KW increased oxygenation; radiation therapy; vascular diseases.
 XX OS Homo sapiens.
 XX Key Locality/Qualifiers
 PH Misc-difference 90
 FT /label= Gln, Lys
 XX US5428007-A.
 PS 27-JUN-1995.
 FT 28-APR-1994; 94US-00235118.
 XX PR 06-OCT-1989; 89US-00417949.
 PR 09-OCT-1992; 92US-00959286.
 XX PA (UYA) UNIV YALE.
 XX PI Baserga SJ, Fischer JJ;
 XX DR 1995-240064/31.
 XX Increasing tissue oxygen in hypoxic cells - by administering a pure
 PT mutant alpha or beta haemoglobin having a low oxygen affinity.
 XX Example 3; Col 5-6; 10pp; English.
 XX AAR89262 is the human beta-globin mutant Val90, Met91, Ser93, Glu94. The
 PT mutant globin can be used to increase tissue oxygenation in hypoxic
 CC cells, to increase oxygenation in tumours to enhance the effects of
 CC radiation therapy or as a blood replacement or treatment in vascular
 CC diseases. (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 58; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LvVYPWTQRF 41
 RESULT 15
 ID AAGG01752 standard; protein; 121 AA.
 XX AAGG01752;
 AC
 XX DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 5833.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Homo sapiens.
 OS EP1033401-A2.
 PN 06-SEP-2000.
 PR 21-FEB-2000; 2000EP-00200610.
 XX 26-FEB-1999; 99US-0122487P.
 XX PD 06-SEP-2000.
 XX (GEST) GENSET.
 PA Dumas Milne Edwards J, Ducleir A, Giordano J;
 PI XX
 DR WPI: 2000-500381/45.
 ID N-PSDB; AAC01758.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 13; SEQ ID NO 5833; 71pp + Sequence Listing; English.
 XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or poly+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranscribed
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' end is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC include
 XX US5428007-A.
 PS 27-JUN-1995.
 DT 04-MAR-1996 (first entry)
 XX DB Human beta-globin mutant Val90, Met91, Ser93, Glu94.
 KW Human beta-globin; mutant Val90, Met91, Ser93, Glu94; hypoxic cells;
 KW increased oxygenation; radiation therapy; vascular diseases.
 XX OS Homo sapiens.
 XX PN US5428007-A.
 XX PR 28-APR-1994; 94US-00235118.
 PR 06-OCT-1989; 89US-00417949.
 PR 09-OCT-1992; 92US-00959286.

CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX

SQ Sequence 121 AA;

Query Match Score 58; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVYPWTQRF 10
| ||||| | | |
Db 33 LVVYPWTQRF 42

Search completed: July 26, 2005, 10:59:46
Job time : 166 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	58	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	100.0	10	2	US-08-627-173-4
2	58	OM protein - protein search, using SW model	100.0	10	2	US-08-627-173-4
3	58	Run on: July 26, 2005, 10:51:13 ; Search time 43 Seconds (without alignments)	100.0	10	2	US-08-627-173-4
4	58	17.360 Million cell updates/sec	100.0	10	2	US-08-627-173-4
5	58	Title: US-09-147-490-1	100.0	10	2	US-08-627-173-4
6	58	Perfect score: 1 LvypwtqrF 10	100.0	10	2	US-08-627-173-4
7	58	Scoring table: BLOSUM62	100.0	10	2	US-08-627-173-4
8	58	Gapext 0.5	100.0	10	2	US-08-627-173-4
9	58	Searched: 513545 seqs, 74649064 residues	100.0	10	2	US-08-627-173-4
10	58	Total number of hits satisfying chosen parameters:	513545			
11	58	Minimum DB seq length: 0				
12	58	Maximum DB seq length: 20000000000				
13	58	Post-processing: Minimum Match 10% Maximum Match 100%				
14	58	Listing First 45 summaries				
15	58	Database : Issued Patents A: 1: /cggn2_6/ptodata/1/iaa/5A_COMBO.pep: 2: /cggn2_6/ptodata/1/iaa/5B_COMBO.pep: 3: /cggn2_6/ptodata/1/iaa/6A_COMBO.pep: 4: /cggn2_6/ptodata/1/iaa/6B_COMBO.pep: 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMBO.pep: 6: /cggn2_6/ptodata/1/iaa/backtitles.pep: *				
16	58	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
17	58	Total number of hits satisfying chosen parameters:	513545			
18	58	Minimum DB seq length: 0				
19	58	Maximum DB seq length: 20000000000				
20	58	Post-processing: Minimum Match 10% Maximum Match 100%				
21	58	Listing First 45 summaries				
22	58	Database : Issued Patents A: 1: /cggn2_6/ptodata/1/iaa/5A_COMBO.pep: 2: /cggn2_6/ptodata/1/iaa/5B_COMBO.pep: 3: /cggn2_6/ptodata/1/iaa/6A_COMBO.pep: 4: /cggn2_6/ptodata/1/iaa/6B_COMBO.pep: 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMBO.pep: 6: /cggn2_6/ptodata/1/iaa/backtitles.pep: *				
23	58	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
24	58	Total number of hits satisfying chosen parameters:	513545			
25	58	Minimum DB seq length: 0				
26	58	Maximum DB seq length: 20000000000				
27	58	Post-processing: Minimum Match 10% Maximum Match 100%				
28	58	Listing First 45 summaries				
29	58	Database : Issued Patents A: 1: /cggn2_6/ptodata/1/iaa/5A_COMBO.pep: 2: /cggn2_6/ptodata/1/iaa/5B_COMBO.pep: 3: /cggn2_6/ptodata/1/iaa/6A_COMBO.pep: 4: /cggn2_6/ptodata/1/iaa/6B_COMBO.pep: 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMBO.pep: 6: /cggn2_6/ptodata/1/iaa/backtitles.pep: *				
30	58	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
31	58	Total number of hits satisfying chosen parameters:	513545			
32	58	Minimum DB seq length: 0				
33	58	Maximum DB seq length: 20000000000				
34	58	Post-processing: Minimum Match 10% Maximum Match 100%				
35	58	Listing First 45 summaries				
36	58	Database : Issued Patents A: 1: /cggn2_6/ptodata/1/iaa/5A_COMBO.pep: 2: /cggn2_6/ptodata/1/iaa/5B_COMBO.pep: 3: /cggn2_6/ptodata/1/iaa/6A_COMBO.pep: 4: /cggn2_6/ptodata/1/iaa/6B_COMBO.pep: 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMBO.pep: 6: /cggn2_6/ptodata/1/iaa/backtitles.pep: *				
37	58	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
38	58	Total number of hits satisfying chosen parameters:	513545			
39	58	Minimum DB seq length: 0				
40	58	Maximum DB seq length: 20000000000				
41	58	Post-processing: Minimum Match 10% Maximum Match 100%				
42	58	Listing First 45 summaries				
43	58	Database : Issued Patents A: 1: /cggn2_6/ptodata/1/iaa/5A_COMBO.pep: 2: /cggn2_6/ptodata/1/iaa/5B_COMBO.pep: 3: /cggn2_6/ptodata/1/iaa/6A_COMBO.pep: 4: /cggn2_6/ptodata/1/iaa/6B_COMBO.pep: 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMBO.pep: 6: /cggn2_6/ptodata/1/iaa/backtitles.pep: *				
44	58	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
45	58	Total number of hits satisfying chosen parameters:	513545			

ALIGNMENTS

RESULT 1
US-08-627-173-4
; Sequence 4, Application US/08627173
; Patent No. 581483

GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 ADDRESS: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPILER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-627-173-4
 FILING DATE: 03-APR-1996
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,892
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acid(s)
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-627-173-4
 Query Match 100.0%; Score 58;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 23, Conservative 0, Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 LVYYPWTQRF 10

Db 1 LvVYPTQRF 10 COUNTRY: U.S.A.
 Zip: 22201-4714 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-535-882A-4

Query Match 100.0%; Score 58; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 Db 1 LVVYPTQRF 10

RESULT 4 US-08-535-882A-26
 Sequence 26, Application US/08535882A
 Patent No. 5939391
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 Zip: 22201-4714 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/627,173
 FILING DATE: 03-APR-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-627-173-26

Query Match 100.0%; Score 58; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 Db 1 LVVYPTQRF 10

RESULT 3 US-08-535-882A-4
 Sequence 4, Application US/08535882A
 Patent No. 5939391
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA

STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-26

Query Match 100.0%; Score 58; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPPTQRF 10
Db 1 LVVYPPTQRF 10

RESULT 5

Sequence 4, Application US/09005546
Patent No. 6030782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

US-09-005-546-26

Query Match 100.0%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPPTQRF 10
Db 1 LVVYPPTQRF 10

RESULT 7

US-10-128-581-4
Sequence 4, Application US/10128581
Patent No. 6610654
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
REGISTRATION NUMBER: 32,205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide
US-09-005-546-4

TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL FOR INHIBITING STEM CELL PROLIFERATION

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
Patent No. 6610654
GENERAL INFORMATION:
APPLICANT: WOLPE, STEPHEN D.
REGISTRATION NUMBER: 32,205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide

RESULT 6
US-09-005-546-26
Sequence 26, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,581

FILING DATE: 24-Apr-2002
 PRIORITY APPLICATION DATA: <Unknown>
 APPLICATION NUMBER: US 09/617,840
 FILING DATE: 17-Jul-2000
 APPLICATION NUMBER: US 09/005,546
 FILING DATE: 12-Jan-1998
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 APPLICATION NUMBER: US 08/316,424
 FILING DATE: 30-SEP-1994
 APPLICATION NUMBER: PCT/US94/03349
 FILING DATE: 29-MAR-1994
 APPLICATION NUMBER: US 08/040,942
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acid
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-128-581-4

Query Match 100.0%; Score 58; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWTQRF 10
 Db 1 LVVYPTWTQRF 10

RESULT 9
 US-08-453-485E-96
 Sequence 96, Application US/08453485E
 ; Patent No. 688155
 ; GENERAL INFORMATION:
 ; APPLICANT: Baxter Biotech Technology Sarl
 ; TITLE OF INVENTION: DNA ENCODING FUSED DI-ALPHA GLOBINS AND USE THEREOF
 ; CURRENT APPLICATION NUMBER: US/08/453,485E
 ; CURRENT FILING DATE: 1995-05-30
 ; PRIOR APPLICATION NUMBER: 1991-11-08
 ; PRIOR FILING DATE: 1991-11-08
 ; PRIOR APPLICATION NUMBER: 07/671,707
 ; PRIOR FILING DATE: 1991-04-01
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 96
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Cheverly (beta phe-> ser)
 US-08-453-485E-96

Query Match 100.0%; Score 58; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWTORE 10
 Db 23 LVVYPTWTQRF 32

RESULT 10
 US-09-352-078-9
 Sequence 9, Application US/09352078
 ; Patent No. 6337314
 ; GENERAL INFORMATION:
 ; APPLICANT: Theregem, Inc.
 ; ATTORNEY: Hoffman, Bernard F.
 ; APPLICANT: Dubnick, Bernard
 ; TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
 ; TREATMENT OF MICROBIAL INFECTIONS
 ; FILE REFERENCE: 1944/1ID99US1
 ; CURRENT APPLICATION NUMBER: US/09/352,078
 ; EARLIER APPLICATION NUMBER: PCT/US98/16746
 ; CURRENT FILING DATE: 1999-07-14
 ; EARLIER FILING DATE: 1998-08-10
 ; EARLIER APPLICATION NUMBER: 60/061,454
 ; EARLIER FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 55
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-352-078-9

Query Match 100.0%; Score 58; DB 3; Length 55;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWTQRF 10

FILING DATE: 03-APR-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/627,173
 FILING DATE: 03-Apr-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/627,173
 FILING DATE: 03-APR-1996
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acid
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-08-832-443C-4

REGISTRATION NUMBER: 30,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 21:
 LENGTH: 74 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-138-922-21

Query Match Score 58; DB 3; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYWPWTORF 10
 Db 2 LVVYWPWTORF 11

RESULT 14
 US-09-138-922-25
 Sequence 25, Application US/09138922
 GENERAL INFORMATION:
 Patent No. 6147202

APPLICANT: Kumar, Ramesh
 APPLICANT: Sharma, Ajay
 APPLICANT: Paulhiac, Clara
 APPLICANT: Khouri-Christiansson, Anastasia P.
 APPLICANT: Midha, Sunita

TITLE OF INVENTION: Production of Human Hemoglobin in
 NUMBER OF INVENTIONS: 26
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/138,922
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,989
 FILING DATE: 11-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-138-922-25

Query Match Score 58; DB 3; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYWPWTORF 10
 Db 2 LVVYWPWTORF 11

RESULT 15
 US-09-513-999C-5833
 Sequence 5833, Application US/09513999C
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J. B.
 APPLICANT: Ducleart, A.
 APPLICANT: Giordano, J.Y.
 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 PATENT NO. 6783961
 CURRENT APPLICATION NUMBER: US/09/513,999C
 FILE REFERENCE: 59-US2.REG
 CURRENT FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: US 60/122,487
 PRIOR FILING DATE: 1999-02-26
 NUMBER OF SEQ ID NOS: 36681
 SEQ ID NO: 5833
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-513-999C-5833

Query Match Score 58; DB 4; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYWPWTORF 10
 Db 33 LVVYWPWTORF 42

Search completed: July 26, 2005, 11:01:18
 Job time : 43 secs

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 10:53:58 ; Search time 156 Seconds
24.935 Million cell updates/sec (without alignments)

Title: US-09-147-490-1

Perfect score: 58

Sequence: 1 Lvvypwtorf 10

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA: *

Database : 1: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaas/fct_new_pub.pep:*

3: /cgn2_6/ptodata/2/pubpaas/us06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaas/bctus_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaas/us08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaas/us09_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaas/us09a_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaas/us09b_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaas/us09c_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaas/us09_d_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaas/us09_e_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaas/us10a_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaas/us10b_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaas/us10c_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaas/us10d_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaas/us10e_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaas/us10_f_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaas/us1a_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaas/us11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/2/pubpaas/us60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaas/us60_PUBCOMB.pep:*

ALIGMENTS

RESULT 1

US-09-147-490-1

; Sequence 1, Application US/09147490

; General Information:

; Applicant: MENDELSON, FREDERICK A.O.

; Applicant: CHAI, SIEW YENN

; Applicant: MOELIER, INGRID

; Applicant: ALDRED, PETER G.

; Applicant: SMITH, IAN A.

; Applicant: LEW, REBECCA A.

; Title of Invention: NEUROACTIVE PEPTIDE

; File Reference: 016786/0215

; Current Application Number: US/09/147,490

; Current Filing Date: 1999-05-03

; Prior Application Number: PCT/AU97/00436

; Prior Filing Date: 1997-07-09

; Prior Application Number: AU P00893

; Number of SEQ ID NOS: 10

; Software: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Beta globin

; OTHER INFORMATION: precursor

US-09-147-490-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	58	100.0	10 9 US-09-147-490-1	Sequence 1, Appli
2	58	100.0	10 14 US-10-128-581-4	Sequence 4, Appli
3	58	100.0	10 15 US-10-453-699-4	Sequence 4, Appli
4	58	100.0	10 16 US-10-776-172-4	Sequence 4, Appli
5	58	100.0	10 17 US-10-485-510A-3	Sequence 4, Appli
6	58	100.0	10 17 US-10-897-005-4	Sequence 4, Appli
7	58	100.0	10 15 US-10-363-616-477	Sequence 47, App
8	58	100.0	146 9 US-09-839-164-4	Sequence 4, Appli
9	58	100.0	146 9 US-09-839-164-8	Sequence 8, Appli
10	58	100.0	146 9 US-09-977-577-15	Sequence 15, Appli
11	58	100.0	146 9 US-09-977-577-16	Sequence 16, App

Query Match 100.0%; Score 58; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0556;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWQRF 10
 Db 1 LVVYPTWQRF 10

RESULT 2
 US-10-128-581-4
 / Sequence 4, Application US/10128581
 / Publication No. US2003010494A1
 / GENERAL INFORMATION:
 / APPLICANT: TSYRLOVA, IRENA D.
 / WOLPE, STEPHEN D.
 / TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL
 / NUMBER OF SEQUENCES: 31
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: NIXON & VANDERHYE P.C.
 / STREET: 1100 NORTH GLEBE ROAD
 / CITY: ARLINGTON
 / STATE: VIRGINIA
 / COUNTRY: U.S.A.
 / ZIP: 22201-4714
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS Word
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/10/463,699
 / FILING DATE: 18-Jun-2003
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 10/128,581
 / FILING DATE: 24-APR-2002
 / APPLICATION NUMBER: US 09/617,840
 / FILING DATE: 17-JUL-2000
 / APPLICATION NUMBER: US 09/005,546
 / FILING DATE: 12-JAN-1998
 / APPLICATION NUMBER: US 08/535,882
 / FILING DATE: 28-SEP-1995
 / APPLICATION NUMBER: US 08/316,424
 / FILING DATE: 30-SEP-1994
 / APPLICATION NUMBER: PCT/US94/03349
 / FILING DATE: 29-MAR-1994
 / APPLICATION NUMBER: US 08/040,942
 / FILING DATE: 31-MAR-1993
 / INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 10 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: <Unknown>
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 / US-10-463-699-4
 Query Match 100.0%; Score 58; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 /
 Qy 1 LVVYPTWQRF 10
 Db 1 LVVYPTWQRF 10

RESULT 4
 US-10-776-172-4
 / Sequence 4, Application US/10776172
 / Publication No. US2004016706A1
 / GENERAL INFORMATION:
 / APPLICANT: TSYRLOVA, IRENA D.
 / WOLPE, STEPHEN D.
 / TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: NIXON & VANDERHYE P.C.
 / STREET: 1100 NORTH GLEBE ROAD
 / CITY: ARLINGTON
 / STATE: VIRGINIA
 / COUNTRY: U.S.A.
 / ZIP: 22201-4714
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS Word
 / CURRENT APPLICATION DATA:
 /

RESULT 3
 US-10-463-699-4
 / Sequence 4, Application US/10463699
 / Publication No. US2004008160A1
 / GENERAL INFORMATION:
 / APPLICANT: TSYRLOVA, IRENA D.
 / WOLPE, STEPHEN D.
 / TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL FOR INHIBITING STEM CELL PROLIFERATION
 / NUMBER OF SEQUENCES: 33

APPLICATION NUMBER: US/10/776,172
 FILING DATE: 12-Feb-2004
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/627,173
 FILING DATE: 03-APR-1996
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 us-10-776-172-4

Qy	1	LVYVPTWQRF	10
Db	1	LVYVPTWQRF	10

RESULT 5
 US-10-485-518A-3
 Sequence 3, Application US/10485518A
 Publication No. US2005020519A1
 GENERAL INFORMATION:
 APPLICANT: Howard Florey Institute of Experimental Physiology and Medicine
 TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE ACTIVITY
 FILE REFERENCE: P42903
 CURRENT APPLICATION NUMBER: US/10/485,518A
 CURRENT FILING DATE: 2004-02-02
 PRIOR APPLICATION NUMBER: PCT/AU02/01034
 PRIOR FILING DATE: 2002-08-02
 PRIOR APPLICATION NUMBER: Australian PR6722
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Ovis aries
 US-10-485-518A-3

Qy	1	LVYVPTWQRF	10
Db	1	LVYVPTWQRF	10

RESULT 6
 US-10-897-005-4
 Sequence 4, Application US/10897005
 Publication No. US20050043218A1
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 WOLPE, STEPHEN D.
 TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBBS ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

Qy	1	LVYVPTWQRF	10
Db	33	LVYVPTWQRF	42

RESULT 8
 US-09-839-164-4

Sequence 4, Application US/09839164
 GENERAL INFORMATION:
 APPLICANT: KOZLOV, VLADIMIR
 TSYRLOVA, IRENA
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 Mb diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/839,164
 FILING DATE: 23-APR-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/477,668
 FILING DATE: 07-JUN-1995
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
 US-09-839-164-4

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

US-09-839-164-4

Query Match 100.0%; Score 58; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWTPRF 10
 Db 32 LVVYPTWTPRF 41

RESULT 9
 US-09-839-164-8

Sequence 8, Application US/09839164
 GENERAL INFORMATION:
 APPLICANT: KOZLOV, VLADIMIR
 TSYRLOVA, IRENA
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 Mb diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 9
 US-09-839-164-8

Sequence 8, Application US/09839164
 GENERAL INFORMATION:
 APPLICANT: KOZLOV, VLADIMIR
 TSYRLOVA, IRENA
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 Mb diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 10
 US-09-977-577-15

Sequence 15, Application US/09977577
 Patent No. US20020155995A1
 GENERAL INFORMATION:
 APPLICANT: MOESTRUP, Soren
 ATTORNEY OR AGENT: MOLLER, Holger J.
 TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/977,577
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: US 60/270,120
 PRIOR FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: DK PA 2001 00039
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: DK PA 2000 01543
 PRIOR FILING DATE: 2000-10-16
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 15
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-977-577-15

Query Match 100.0%; Score 58; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTWTPRF 10
 Db 32 LVVYPTWTPRF 41

RESULT 11
 US-09-977-577-16

Sequence 16, Application US/09977577
 Patent No. US20020155995A1
 GENERAL INFORMATION:
 APPLICANT: MOESTRUP, Soren

APPLICANT: MOLLER, Holger J.
 FILE REFERENCE: MOESTRUP=1A
 CURRENT APPLICATION NUMBER: US/09/977,577
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: US 60/270,120
 PRIOR FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: DK PA 2001 00039
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: DK PA 2000 01543
 PRIOR FILING DATE: 2000-10-16
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 16
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-977-577-16

Query Match Score 58; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 14
 US-10-085-853-33
 ; Sequence 33, Application US/10085853
 ; Publication No. US20020194613A1

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 15
 US-10-085-853-33
 ; Sequence 33, Application US/10085853
 ; Publication No. US20020194613A1

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 16
 US-10-085-853-33
 ; Sequence 33, Application US/10085853
 ; Publication No. US20020194613A1

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 17
 US-09-977-577-17
 ; Sequence 17, Application US/09977577
 ; Patent No. US20020155995A1

GENERAL INFORMATION:
 APPLICANT: MOESTRUP, Soren
 APPLICANT: MOLLER, Holger J.

TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES
 CURRENT APPLICATION NUMBER: US/09/977,577
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: US 60/270,120
 PRIOR FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: DK PA 2001 00039
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: DK PA 2000 01543
 PRIOR FILING DATE: 2000-10-16
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 17
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-977-577-17

Query Match Score 58; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 18
 US-10-085-853-33
 ; Sequence 33, Application US/10085853
 ; Publication No. US20020194613A1

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 19
 US-10-085-853-33
 ; Sequence 33, Application US/10085853
 ; Publication No. US20020194613A1

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 20
 US-10-085-853-33
 ; Sequence 20, Application US/09977577
 ; Patent No. US20020155995A1

GENERAL INFORMATION:
 APPLICANT: MOESTRUP, Soren
 APPLICANT: MOLLER, Holger J.

TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES
 CURRENT APPLICATION NUMBER: US/09/977,577
 CURRENT FILING DATE: 2001-10-16

FOR INHIBITING STEM CELL PROLIFERATION

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA

ZIP: 22201-4714
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,581
FILING DATE: 24-APR-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/617,840
FILING DATE: 17-JUL-2000

APPLICATION NUMBER: US 09/005,546
FILING DATE: 12-JAN-1998

APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995

APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994

APPLICATION NUMBER: PCT/US94/03349
FILING DATE: 29-MAR-1994

APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: Linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-128,581-23

Query Match 100.0% Score 58: DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LVVVPTQRF	10
Db	32	LVVVPTQRF	41

Search completed: July 26, 2005, 11:04:00
Job time : 157 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: July 26, 2005, 10:50:07 ; Search time 39 Seconds
 (without alignments)
 24.671 Million cell updates/sec

Title: US-09-147-490-1

Perfect score: 58

Sequence: 1 LVVYPTQRF 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 10%

Listing First 45 summaries

Database : PIR 79:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:
 * * * *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	58	100.0	61	4	I65317	hemoglobin delta chain - human (fragment)
2	58	100.0	61	4	I52502	C;Species: Homo sapiens (man)
3	58	100.0	110	4	I46172	C;Date: 12-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 09-Jul-2004
4	58	100.0	122	2	A05304	C;Accession: I65317 R.Liu, J.Z.; Harano, T.; Lanclos, K.D.; Huisman, T.H.
5	58	100.0	141	1	HBMF	Biochim. Biophys. Acta 909, 208-212, 1987
6	58	100.0	141	1	HBSHCR	A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-1
7	58	100.0	141	1	HBGTC	A;Reference number: I52502; MUID:87299720; PMID:3620470
8	58	100.0	142	1	HBSHC	A;Status: translated from GB/EMBL/DBJ
9	58	100.0	145	1	HBBOB	A;Molecule type: DNA
10	58	100.0	145	1	HBBOP	A;Residues: 1-61 <LIU>
11	58	100.0	145	1	HBBOF	A;Cross-references: UNIPROT:Q14484; GB:M25660; NID:9183863; PID:9183154.1; PMID:9183864
12	58	100.0	145	1	HBBOK	A;Note: this sequence was not determined in this report
13	58	100.0	145	1	HBBOKA	C;Genetics:
14	58	100.0	145	1	HBDE3	RESULT 2
15	58	100.0	145	1	HBEKN	I52502 R.Liu, J.Z.; Harano, T.; Lanclos, K.D.; Huisman, T.H.
16	58	100.0	145	1	HBGTA	Biochim. Biophys. Acta 909, 208-212, 1987
17	58	100.0	145	1	HBGTF	A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-1
18	58	100.0	145	1	HBSHA	A;Reference number: I52502; MUID:87299720; PMID:3620470
19	58	100.0	145	1	HBSHB	A;Accession: I52502 A;Status: translated from GB/EMBL/DBJ
20	58	100.0	145	1	HBYA2	A;Molecule type: DNA
21	58	100.0	145	1	HGSN	A;Residues: 1-61 <LIU>
22	58	100.0	145	2	S13609	A;Cross-references: UNIPROT:Q14484; GB:M25660; NID:9183863; PID:9183153.1; PMID:9183857
23	58	100.0	145	2	C25727	A;Note: this sequence was not determined in this report
24	58	100.0	145	2	B58794	C;Genetics:
25	58	100.0	146	1	HDGI	A;Gene: GDB:HB
26	58	100.0	146	1	B61434	A;Cross-references: GDB:119297
27	58	100.0	146	1	HBBAG	A;Map position: 11p15.4-11p15.4
28	58	100.0	146	1	HBBAM	A;Introns: 31/3
29	58	100.0	146	1	HBBAY	

ALIGNMENTS

Query Match Similarity 100.0%; Score 58; DB 4; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.0029; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 3
 I46172 hypothetical hemoglobin psi-beta-Z pseudogene - goat (fragment)
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Accession: I46172 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
 R;Ceary, M.L.; Schon, E.A.; Lingrel, J.B.
 Cell 26: 181-180, 1981.
 A;Title: Two related pseudogenes are the result of a gene duplication in the goat beta-g
 A;Reference number: I46172; PMID:82137052; PMID:7332927
 A;Accession: I46172
 A;Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene
 A;Residues: 1-110 <CLE>
 A;Cross-references: EMBL:V00154; NID:9965; PIDN:CAB23469.1; PID:9966
 C;Keywords: pseudogene
 A;GenBank: 11/3; 18/3; 29/2; 103/3

Query Match Similarity 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0051; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40

RESULT 4
 A05304 hemoglobin beta-1 chain - Indian spiny-tailed lizard (tentative sequence) (Fragments)
 C;Species: Uromastyx hardwickii (Indian spiny-tailed lizard)
 C;Accession: A05304 #sequence_revision 05-Jun-1987 #text_change 12-Jul-2004
 R;Naury, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jornvall, H.
 FEBS Lett. 162: 290-295, 1983
 A;Reference number: A91314; PMID:84029159; PMID:6628672
 A;Accession: A05304
 A;Molecule type: protein
 A;Residues: 1-122 <NAQ>
 A;Cross-references: UNIPROT:P18991
 A;Note: the peptides were positioned by homology
 C;Keywords: chromoprotein; globin; globin homology; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-122/Domain: Globin homology (Fragments) <GLB>
 F;80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 58; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 0.0057; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 5
 HBMF hemoglobin beta-C chain - mouflon (tentative sequence)
 C;Species: Ovis orientalis musimon, Ovis ammon musimon (mouflon)
 C;Accession: A02323; A02396
 R;Wilson, J.B.; Miller, A.; Huisman, T.H.J.

Biochem. Genet. 4, 677-688, 1970
 A;Title: Production of hemoglobin C in the mouflon (*Ovis musimon pallas*, 1811) and the k
 ptides from the beta(B) and beta(C) chains
 A;Reference number: A90232
 A;Molecule type: protein
 A;Residues: 1-141 <WIL>
 C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
 C;Superfamily: Globin; Globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;1-141/Domain: globin homology <GLB>
 F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 58; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 0.0066; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 LVVYPWTQRF 10
 Db 27 LVVYPWTQRF 36

RESULT 6
 HBHCR hemoglobin beta-C chain - aoudad (tentative sequence)
 C;Species: Ammotragus lervia (aoudad, Barbary sheep)
 C;Accession: B90232; A02396 #sequence_revision 30-Sep-1993 #text_change 12-Jul-2004
 R;Wilson, J.B.; Miller, A.; Huisman, T.H.J.
 Biochem. Genet. 4, 677-688, 1970
 A;Title: Production of hemoglobin C in the mouflon (*Ovis musimon pallas*, 1811) and the k
 ptides from the beta(B) and beta(C) chains
 A;Reference number: A90232; PMID:71089262; PMID:5496230
 A;Molecule type: protein
 A;Residues: 1-141 <WIL>
 C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
 C;Superfamily: Globin; Globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;1-141/Domain: globin homology <GLB>
 F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 58; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 0.0066; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 LVVYPWTQRF 10
 Db 27 LVVYPWTQRF 36

RESULT 7
 HBGTC hemoglobin beta-C chain - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Accession: B02396; I46277; A02396
 R;Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.
 Cell 27, 359-369, 1981
 A;Title: Structure and evolution of goat gamma-, beta(c)- and beta(a)-globin genes: three
 A;Accession number: A90817; PMID:6277503
 A;Molecule type: DNA
 A;Residues: 1-141 <SCH>
 A;Cross-references: UNIPROT:PO2078; GB:M15389
 A;Note: initiator Met not shown
 R;Haynes, J.R.; Rostek, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; Ling
 J. Biol. Chem. 255, 6355-6367, 1980
 A;Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive

A;Reference number: I46273; MUID:80227766; PMID:6248519
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 66-93, 'XX', 96-115, 'XX', 118-134 <HAY>
A;Cross-references: GB:K00662; NID:9164154; PID:9164158
C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
A;Introns: 26/2; 100/3
C;Superfamily: globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
P;1-141/Domain: Globin homology <GLB>
P;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
P;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted
Query Match Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0066%; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LIVVPTQRF 10
Db 27 LIVVPTQRF 36

RESULT 8
hemoglobin beta-C chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: 30-Sep-1993 #Sequence-revision 30-Jan-1998 #text_Change 12-Jul-2004
R;Garner, K.J.; Lingrel, J.B.
J. Mol. Evol. 28, 175-184, 1989
A;Title: A comparison of the beta (A)- and beta (B)-globin gene clusters of sheep.
A;Reference number: S10073; MUID:89178744; PMID:2494347
A;Accession: S10074
A;Molecule type: DNA
A;Residues: 1-142 <GAR>
A;Cross-references: UNIPROT:PO2079; EMBL:X14728; NID:g1212; PIDN:CAA32850.1; PID:g1213
A;Note: the authors translated the codon GTC for residue 30 as Ala
R;Boyer, S.H.; Hatchaway, P.; Pacasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.
J. Biol. Chem. 242, 2211-2232, 1967
A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep he
A;Reference number: A92027; MUID:67134347; PMID:6022868
A;Accession: B92027
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'ZB
A;Experimental source: Dorset breed
R;Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huisman, T.H.J.
Arch. Biochem. Biophys. 115, 385-400, 1966
A;Title: The structure of sheep hemoglobins. II. The amino acid composition of the trypt
A;Reference number: A90045
A;Accession: A90045
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'ZB
A;Experimental source: Rambouillet breed
A;Note: there are several discrepancies between the sequence in this paper and that give
C;Comment: This beta-C chain is produced when anemia is experimentally induced.
A;Introns: 26/2; 100/3
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to form
A;Function: in erythrocytes binds and transports molecular oxygen from lung to tissue
C;Superfamily: globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
P;1-142/Domain: Globin homology <GLB>
P;2-142/Product: hemoglobin beta-C chain #status experimental <MAT>
P;59/Binding site: oxygen (His) (distal axial ligand) #status predicted
P;88/Binding site: heme iron (His) (proximal axial ligand) #status predicted
Query Match Score 58; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.0066%; Gaps 0; Mismatches 0; Indels 0; Gaps 0;

C;Genetics:
A;Introns: 28/2; 102/3
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to form hemoglobin beta-A chain - banteng (tentative sequence)
C;Function:
A;Description: in erythrocytes binds and transports molecular oxygen from lung to tissue
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F;2-145/Domain: globin homology <GLB>
F;3-140/Product: Lvvypmtqrp 10 #status experimental <OP19>
F;3-140/Product: VV-hemorphin-7 #status experimental <OP19>
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 Lvvypmtqrp 10
Db 31 Lvvypmtqrp 40

RESULT 12
HBBOG
hemoglobin beta chain - gayal
C;Species: Bos taurus frontalis (gayal)
C;Date: 17-May-1985 #text_change 17-May-1985 #text_change 12-Jul-2004
C;Accession: A02389
R;Laihantluanga, R.; Braunitzer, G.
R;Nanikawa, T.; Takemoto, O.; Takahashi, K.
BioChem. Genet. 21: 787-796, 1983
A;Title: Hemoglobin Bali (bovine): beta(A)18(B1)Lys -> His: one of the "missing links" b
A;Reference number: A02388; MUID:6626147
A;Accession: A02388
A;Molecule type: protein
A;Residues: 1-145 <NAM>
A;Cross-references: UNIPROT:P043446
A;Experimental source: Hereford breed
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;2-145/Domain: globin homology <GLB>
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 Lvvypmtqrp 10
Db 31 Lvvypmtqrp 40

RESULT 13
HBBOKA
hemoglobin beta chain - greater kudu
C;Species: Tragelaphus strepsiceros (greater kudu)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 12-Jul-2004
C;Accession: A02391
R;Rodewald, K.; Wiesser, H.; Braunitzer, G.
R;Hoppe-Seyler 366, 395-402, 1985
Bio. Chem. Hoppe-Seyler 366, 395-402, 1985
A;Title: Primary structure of the hemoglobins from the greater kudu antelope (Tragelaphus
A;Reference number: A90684; MUID:85273893; PMID:4026393
A;Accession: A02391
A;Molecule type: protein
A;Residues: 1-145 <R0D>
A;Cross-references: UNIPROT:P04245
A;Note: there are two alleles for the beta chain, one having the sequence shown and the c
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;2-145/Domain: globin homology <GLB>
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;

Qy 1 Lvvypmtqrp 10
Db 31 Lvvypmtqrp 40

RESULT 11
HBBOF
hemoglobin beta chain, fetal - bovine
N;Alternate names: hemoglobin gamma chain
C;Species: Bos primigenius taurus (cattle)
C;Accession: A93504; A90549; A02398
R;Schimenti, J.C.; Duncan, C.H.
Nucleic Acids Res. 12, 1641-1655, 1984
A;Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats
A;Reference number: A93504; PMID:34144058; PMID:6322113
A;Accession: A93504
A;Molecule type: DNA
A;Residues: 1-145 <SCH>
A;Cross-references: UNIPROT:P02081; GB:X00354; NID:9392; PID:CAA25101.1; PMID:9393
R;Babin, D.R.; Schroeder, W.A.; Shelton, J.R.; Robberson, B.
Biochemistry 5, 1297-1310, 1996
A;Title: The amino acid sequence of the gamma chain of bovine fetal hemoglobin.
A;Reference number: A90549; PMID:67089183; PMID:5958205
A;Accession: A90549

Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40

RESULT 14

HBDE3
 hemoglobin beta-III chain - Virginia white-tailed deer
 C;Species: Odocoileus virginianus virginianus (Virginia white-tailed deer)
 C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 12-Jul-2004
 C;Accession: A02393
 R;Shimizu, K.; Wong, S.C.; Wilson, J.B.; Lam, H.; Reynolds, A.B.; Singh, P.; Huisman, T.
 Hemoglobin 7, 15-45, 1983
 A;Title: The primary sequence of the beta chain of Hb type III of the Virginia white-tail
 deer hemoglobin, types II, IV, V, and VII, and relationships between intermolecular con
 A;Reference number: A02393; MUID:83185439; PMID:6841126
 A;Accession: A02393
 A;Molecule type: protein
 A;Residues: 1-145 <SH1>
 A;Cross-references: UNIPROT:P02074
 C;Comment: This chain is one of five beta chain alleles.
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;2-145/Domain: Globin homology <GLB>
 F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40

RESULT 15

HBERN
 hemoglobin beta chain - European moose
 C;Species: Alces alces ales (European moose, elk)
 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 12-Jul-2004
 C;Accession: A02392
 R;Aschauer, H.; Wiesner, H.; Braunitzer, G.
 Hoppe-Seyler's Z. Physiol. Chem. 365, 1321-1330, 1984
 A;Title: Zur intrinsischen Sauerstoffaffinitaet: die Primaerstruktur eines weiteren Rumi
 A;Reference number: A91729; MUID:85078042; PMID:6510988
 A;Accession: A02392
 A;Molecule type: protein
 A;Residues: 1-145 <ASC>
 A;Cross-references: UNIPROT:P02073
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;2-145/Domain: Globin homology <GLB>
 F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40

Search completed: July 26, 2005, 11:00:29
 Job time : 39 secs

This Page Blank (uspto)

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 10%

Listing first 45 summaries

Database : UniProt 03:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	17	Q9UM85	Q9UM85 homo sapien
2	58	100.0	59	Q9BXA2	Q9BXA2 homo sapien
3	58	100.0	61	Q1484	Q1484 homo sapien
4	58	100.0	61	Q1485	Q1485 homo sapien
5	58	100.0	61	Q9UBV6	Q9UBV6 homo sapien
6	58	100.0	89	Q9UP81	Q9UP81 homo sapien
7	58	100.0	101	Q14476	Q14476 homo sapien
8	58	100.0	101	Q14477	Q14477 homo sapien
9	58	100.0	105	Q8IQU9	Q8IQU9 homo sapien
10	58	100.0	105	Q8IZ0	Q8IZ0 homo sapien
11	58	100.0	105	Q67054	Q67054 homo sapien
12	58	100.0	105	Q6J127	Q6J127 homo sapien
13	58	100.0	105	Q6V0K9	Q6V0K9 homo sapien
14	58	100.0	105	Q9BWU5	Q9BWU5 homo sapien
15	58	100.0	111	Q9BKV6	Q9BKV6 homo sapien
16	58	100.0	113	Q02770	Q02770 callithrix
17	58	100.0	115	Q9GZL9	Q9GZL9 homo sapien
18	58	100.0	123	Q14474	Q14474 homo sapien
19	58	100.0	125	Q13072	Q13072 callithrix
20	58	100.0	125	Q28799	Q28799 pan troglodytes
21	58	100.0	128	Q9UK54	Q9UK54 homo sapien
22	58	100.0	129	Q9UNL6	Q9UNL6 homo sapien
23	58	100.0	133	Q28852	Q28852 ovis aries
24	58	100.0	141	HBBC_AMMLB	HBBC_AMMLB
25	58	100.0	141	HBBC_CAPII	HBBC_CAPII
26	58	100.0	141	HBBC_OVIMD	HBBC_OVIMD
27	58	100.0	141	HBBC_SHEBP	HBBC_SHEBP
28	58	100.0	141	HBB_CALGE	HBB_CALGE
29	58	100.0	142	Q95233	Q95233 perodiculus
30	58	100.0	145	HBBA_BOSJA	HBBA_BOSJA
31	58	100.0	145	HBBA_CAPIT	HBBA_CAPIT

ALIGNMENTS

RESULT 1					
Q9UM85 PRELIMINARY; PRT; 17 AA.					
ID	Q9UM85				
AC	Q9UM85;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DB	Beta-globin protein (Fragment).				
GN	Name=beta-globin;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID	9606;				
RN	[1]				
SEQUENCE FROM N.A.					
RX	Medline=96552914; PubMed=8718696;				
RA	Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.,				
RT	"A novel intrachromosomal rearrangement in the beta-globin gene found in an African-American family.";				
RT	RT in Hemoglobin 19:375-388(1995).				
RL	DR S82267; ARD14420.1; -.				
DR	HSSP; P02023; IC7C.				
FT	NON_TER 17				
SQ	SEQUENCE 17 AA; 2104 MW; 419775BE5260504 CRC64;				
Query Match 100 %; Score 58; DB 2; Length 17;					
Best Local Similarity 100 %; Pred. No. 0.0034;	Mismatches 0;	Indels 0;	Gaps 0;		
Matches 10; Conservative 0;					
Qy 1 LVVYPTQRF 10					
Db 2 LVVYPTQRF 11					
RESULT 2					
Q9BXA2 PRELIMINARY; PRT; 59 AA.					
ID	Q9BXA2				
AC	Q9BXA2;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Beta-globin (Fragment).				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID	=5606;				
RN	[1]				
SEQUENCE FROM N.A.					
RA	Kutlar F., Aquilina P.M., Glendinning M., Kutlar A.; Submitted (FEB-2001) to the EMBL/GenBank/DDJB databases.				
RL	DR AF348448; AAK30154.1; -.				
DR	HSSP; P02023; 1DXT.				
DR	GO; GO:0005333; C:hemoglobin complex; IEA.				
DR	GO; GO:0005344; F:oxygen transporter activity; IEA.				

DR PFam; PF00042; Globin; 1.
 DR PRINTS; PRO0814; BETHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport.
 FT NON-TER 61
 SQ SEQUENCE 61 AA; 6691 MW; 905E99BF2C12A13 CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQUENCE 59 AA; 59 MW; 128EF2C12A13A9D3 CRC64;
 Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 4
 Q14485 PRELIMINARY; PRT; 61 AA.
 ID Q14485 PRELIMINARY;
 AC Q14485; PRT; 61 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Delta-hemoglobin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87299720; PubMed=1620470; DOI=10.1016/0167-4781(87)90079-0;
 RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
 RT "The beta-delta crossover leading to the beta delta hybrid gene of
 hemoglobin P-Nilotic is located within the 54 base-pairs of the 5' end of
 exon 2 or between codons 31 and 50".
 RT [1] Between codons 31 and 50".
 RL Biochim. Biophys. Acta 909:208-212(1987).
 RP EMBL; M25651; AA53154.1; -.
 DR PIR; I65317; I63317.
 DR HSSP; P02023; 1DXT.
 DR GO; GO-0005833; C:hemoglobin complex; IEA.
 DR GO; GO-0005344; F:oxygen transport activity; IEA.
 DR GO; GO-0015671; P:oxygen transport; IEA.
 DR InterPro; IPR02337; Beta haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR03050; Globin_like.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PS01033; GLOBIN; 1.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport.
 FT NON-TER 61
 SQ SEQUENCE 61 AA; 6691 MW; D5DC4F2CC2DDF822 CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQUENCE 59 AA; 59 MW; 128EF2C12A13A9D3 CRC64;
 Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 5
 Q9UBV6 PRELIMINARY; PRT; 61 AA.
 ID Q9UBV6 PRELIMINARY;
 AC Q9UBV6; PRT; 61 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-globin (Fragment).
 GN Name=HBB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR HSSP; P02023; 1DXT.
 DR GO; GO:005833; C:hemoglobin complex; IEA.
 DR GO; GO:005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0015671; P:oxygen transport; IEA.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR009050; Globin_like.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PR00814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 Heme; Oxygen transport; Transport.
 NON_TER 101_101
 SEQUENCE 101 AA; 10928 MW; F54BFDB224B5DB0F CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 0.021; P:mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; N mismatches 0; O
 Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42
 RESULT 9
 Q8IUL9 PRELIMINARY; PRT; 105 AA.
 AC Q8IUL9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hemoglobin beta chain variant Hb.Sinai-Bel Air (Fragment).
 GN Name-HBB;
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole blood;
 RA Kutlar F., Holley L., Elam D., Dutton C., Dainer B.M., Kutlar A.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP040397; AN016468; 1; -.
 DR HSSP; P02023; 1DXT.
 DR GO; GO:005833; C:hemoglobin complex; IEA.
 DR GO; GO:005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0015671; P:oxygen transport; IEA.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR009050; Globin_like.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PR00814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 Heme; Oxygen transport; Transport.
 NON_TER 105 AA; 11548 MW; F03ABCCP853A4FFF CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.021; P:mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; N mismatches 0; O
 Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42
 RESULT 10
 Q8IZ10 PRELIMINARY; PRT; 105 AA.
 ID Q8IZ10
 AC Q8IZ10
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DR HSSP; P02023; 1DXT.
 DR GO; GO:005833; C:hemoglobin complex; IEA.
 DR GO; GO:005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0015671; P:oxygen transport; IEA.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR009050; Globin_like.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PR00814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 Heme; Oxygen transport; Transport.
 NON_TER 105 AA; 11459 MW; FADD4606FAA4F614 CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.021; P:mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; N mismatches 0; O
 Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

Db 33 LVVYPWTQRF 42

RESULT 12

Q6J1Z7 PRELIMINARY; PRT; 105 AA.

AC Q6J1Z7; 06J1Z7; 05-JUL-2004 (TREMBLrel. 27, Created) 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update).

DB Hemoglobin beta (Fragment).

GN Name=HBB;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

OX

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Atabay E.O., Blam D., Nechtmann J., Kutlar A., Kutlar F.; Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY605052; AAT36651.1; -.

DR HSSP; P02023; 1BAB.

DR GO; GO:0005833; C:hemoglobin complex; IEA.

DR CO; GO:0005344; P:oxygen transporter activity; IEA.

DR GO; GO:0015671; P:oxygen transport; IEA.

DR InterPro; IPR000971; Beta haem.

DR InterPro; IPR0005050; Globin.

DR InterPro; IPR00042; Globin_1.

DR PFAM; PF000814; Betahaem.

DR PROSITE; PS01033; GLOBIN_1.

DR Heme; Oxygen transport; Transport.

KW Heme; Oxygen transport; Transport.

FT SEQUENCE 105 AA; 11446 MW; 443ABBA3F54BF8E2 CRC64;

SQ

Query Match Score 58; DB 2; Length 105; Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 33 LVVYPWTQRF 42

RESULT 13

Q6V0K9 PRELIMINARY; PRT; 105 AA.

AC Q6V0K9; 06V0K9; 05-JUL-2004 (TREMBLrel. 27, Created) 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update).

DB Mutant hemoglobin beta chain (Fragment).

GN Name=HBB;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

OX

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Kutlar F., Mirnow D., Glendinning M., Kutlar A.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY356351; AQQ63175.1; -.

DR HSSP; P02023; 1BAB.

DR GO; GO:0005833; C:hemoglobin complex; IEA.

DR GO; GO:0005344; P:oxygen transporter activity; IEA.

DR GO; GO:0015671; P:oxygen transport; IEA.

DR InterPro; IPR000971; Globin.

DR InterPro; IPR0005050; Globin_like.

DR Pfam; PF000814; Globin_1.

DR PROSITE; PS01033; GLOBIN_1.

DR Heme; Oxygen transport; Transport.

KW Heme; Oxygen transport; Transport.

FT SEQUENCE 105 AA; 11501 MW; 8143C84D90C01687 CRC64;

SQ

Query Match Score 58; DB 2; Length 105; Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 33 LVVYPWTQRF 42

RESULT 14

Q9BWU5 PRELIMINARY; PRT; 105 AA.

AC Q9BWU5; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update).

DE Mutant hemoglobin beta chain (Fragment).

GN Name=HBB;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

OX

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Kutlar F., Leithner C., Briscoe J., Kutlar A.; Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY027800; AAK15811.1; -.

DR HSSP; P02023; 2BBS.

DR GO; GO:0005833; C:hemoglobin complex; IEA.

DR GO; GO:0005344; P:oxygen transporter activity; IEA.

DR GO; GO:0005344; P:oxygen transport; IEA.

DR GO; GO:0015671; P:oxygen transport; IEA.

DR InterPro; IPR002337; Beta haem.

DR InterPro; IPR000971; Globin.

DR InterPro; IPR0005050; Globin_like.

DR Pfam; PF000814; Globin_1.

DR PROSITE; PS01033; GLOBIN_1.

DR Heme; Oxygen transport; Transport.

KW Heme; Oxygen transport; Transport.

FT SEQUENCE 105 AA; 11501 MW; 8143C84D90C01687 CRC64;

SQ

Query Match Score 58; DB 2; Length 105; Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 33 LVVYPWTQRF 42

RESULT 15

Q9BWV6 PRELIMINARY; PRT; 111 AA.

AC Q9BWV6; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update).

DE Mutant beta globin.

GN Name=HBB;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

OX

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Kutlar F., Mirnow D., Glendinning M., Kutlar A.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY356351; AQQ63175.1; -.

DR HSSP; P02023; 1BAB.

DR GO; GO:0005833; C:hemoglobin complex; IEA.

DR GO; GO:0005344; P:oxygen transporter activity; IEA.

DR GO; GO:0015671; P:oxygen transport; IEA.

DR InterPro; IPR002337; Beta haem.

DR InterPro; IPR000971; Globin.

DR InterPro; IPR0005050; Globin_like.

RP SEQUENCE FROM N.A.
 RC TISSUE=Whole blood;
 RA Kutluar F., Adekunle A.D., Leithner C., Kurtlar A.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY027509; AA20080.1; -.
 DR HSSP; P02023; 1DXT.
 DR GO; GO:0005344; :hemoglobin complex; IEA.
 DR GO; GO:0005833; :oxygen transporter activity; IEA.
 DR GO; GO:0015671; P:oxygen transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR000971; GlobIn.
 DR InterPro; IPR009050; Globin_like.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PR00814; BETAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport.
 KW SEQUENCE 111 AA; 12234 MW; 8932F924B5B3903A CRC64;
 SQ

Query Match 100.0%; Score 58; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LVYPWTQRF	10
Db	33	Lvypwtqr	42

Search completed: July 26, 2005, 10:56:54
 Job time : 179 secs